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Construction of thiostrepton-inducible, high-copy-number expression vectors for use in *Streptomyces* spp.

(*tipA*: flounder growth hormone; β-keto acyl synthase; *redD*: His₆ tag; *Streptomyces lividans*; *Streptomyces coelicolor*)

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SUMMARY

A high-copy-number plasmid expression vector (pIJ6021) was constructed that contains a thiostrepton-inducible promoter, *PtipA*, from *Streptomyces lividans* 66. The promoter and ribosome-binding site of *tipA* lie immediately upstream from a multiple cloning site (MCS) which begins with a NdeI site (5′-CATATG) that includes the *tipA* translational start codon (ATG), allowing the synthesis of native proteins. Transcriptional terminators occur just upstream from *PtipA* and immediately downstream from the MCS. To demonstrate the utility of pIJ6021, two streptomycete genes and a growth hormone-encoding gene from flounder (*Paralichthys olivaceus*) were cloned in the vector and expressed in *S. lividans* or *S. coelicolor A3(2)*. A derivative of pIJ6021, pIJ4123, has a unique NdeI site positioned downstream from a nucleotide sequence that encodes a His₆ sequence and thrombin cleavage site. pIJ4123 can be used to produce His₆-tagged fusion proteins that can be readily purified by Ni²⁺-affinity chromatography; if necessary, the His₆ tag can be removed by digestion with thrombin. The vectors contain a kanamycin-resistance-encoding gene for the selection of transformants.

INTRODUCTION

Attempts to over-produce native and heterologous proteins in streptomycetes have relied largely on the use of hcn vectors with strong, constitutively expressed promoters (for reviews, see Engels and Koller, 1992; Anné and Van Mellaert, 1993; Molnár, 1994). For proteins that may be deleterious to cell growth, or where there may be a need to control the expression of a cloned gene for experimental purposes, a regulatable system is desirable. Transcription of the chromosomal *tipA* gene of *Streptomyces lividans* 66 (John Innes Centre strain 1326) is apparently induced at least 200-fold by low levels of the antibiotic thiostrepton (Th; Murakami et al., 1989); when cloned on a mcn plasmid in *S. ambofaciens*, transcription from the *tipA* promoter (*p*tipA) appeared to be induced at least 60-fold upon addition of Th (Kuhstoss and Rao, 1991). *tipA* was cloned and characterised (Murakami et al., 1989) and the regulation of *p*tipA studied in detail (Holmes et al., 1993). *p*tipA has been used to regulate gene expression in integrative vectors (Smokvina et al., 1990), and in mcn and hcn plasmids (Murakami et al., 1989; Kuhstoss and Rao, 1991; Holt et al., 1992). Here, we describe the construction of two hcn, *p*tipA-based promoters (for reviews, see Engels and Koller, 1992; Anné and Van Mellaert, 1993; Molnár, 1994).
vectors, pIJ6021 and pIJ4123. pIJ4123 can be used to produce His-tagged fusion proteins that can be readily purified by Ni²⁺-affinity chromatography (Hoffmann and Roeder, 1991, and references therein). To demonstrate the utility of pIJ6021, two streptomycete genes and a growth hormone gene from the flatfish Paralichthys olivaceus (commonly known as flounder) were expressed in S. lividans or S. coelicolor A3(2).

EXPERIMENTAL AND DISCUSSION

(a) Construction of pIJ6021

A 115-bp synthetic tipA fragment (corresponding to nt 4–119 of the published tipA sequence; Holmes et al., 1993) was made that contained a Ndel site (5'-CATATG) overlapping the tipA translational start codon (ATG). This fragment was inserted into a derivative of the hcn plasmid pIJ487 (50–100 copies per chromosome; T. Kieser, personal communication; Ward et al., 1986) to give pIJ6021 (Fig. 1). pIJ6021 contains a MCS to facilitate fragment insertion. The t₂₆ transcriptional terminator of oop RNA from phage λ (Hayes and Szybalski, 1973; Zukowski and Miller, 1986) occurs upstream from ptipA to prevent transcriptional read-through from the vector and to maximise the induction ratio upon addition of Th. A transcriptional terminator from phage ld (td₂₆; Gentz et al., 1981; Ward et al., 1986) is located downstream from the MCS to prevent potentially deleterious transcription of vector sequences from ptipA. A Km⁸ gene (kan) from Micromonospora echinospora (C. Nojiri, personal communication) allows selection of transformants, and the Th⁸ gene (tsr) from S. aureus provides resistance to Th upon induction of ptipA with the antibiotic. To assess the utility of pIJ6021, three functionally diverse genes were inserted in the vector, and their expression levels assessed before and after induction of ptipA with Th.

(b) Application of pIJ6021

The tcmK gene of S. glaucescens GLA.0 encodes a 45-kDa β-keto acyl synthase that plays an early role in the synthesis of the polyketide antibiotic tetracenomycin C (ORF1 of Bibb et al., 1989; Gramajo et al., 1991). A 1.7-kb Ndel-tcmK-HindIII fragment, with the Ndel site overlapping the start codon of tcmK, was inserted between the Ndel and HindIII sites of pIJ6021 to give pIJ6024. Coomassie blue staining following SDS-PAGE revealed a protein of approx. 50 kDa (TcmK migrates more slowly than expected upon SDS-PAGE; Gramajo et al., 1991) in induced S. lividans 1326[pIJ6024] that was not apparent in uninduced cultures (Fig. 2A, upper panel). Western analysis using Ab raised to a synthetic oligopeptide corresponding to an internal segment of TcmK (Gramajo et al., 1991) confirmed that the 50-kDa protein was TcmK (Fig. 2A, lower panel), and also revealed lower amounts of the protein in uninduced S. lividans 1326[pIJ6024]; a corresponding band was not detected in S. lividans 1326[pIJ6021] grown with and without Th (Fig. 2A, lower panel).

Mature FGH is a 20-kDa protein derived from the primary translation product by removal of a 17-aa signal peptide that is normally required for secretion (Watahiki et al., 1989). The PCR (Erlich, 1989) was used to place a NdeI site at the beginning of the coding region of the mature FGH and a BamHI site just beyond the 3’ end of the coding region. At the same time, codons 2 and 4 of the truncated fgh were changed so that the first 12 codons corresponded to synonymous codons that are used most frequently in streptomycete genes (Wright and Bibb, 1992) (expression of high-G+C streptomycete genes in Escherichia coli was enhanced by changing the first few N-terminal codons to the synonyms most frequently used in highly expressed E. coli genes; Gramajo et al., 1991; Angell et al., 1992). The 550-bp Ndel-fgh-BamHI fragment was inserted in pIJ6021 that had been cleaved with Ndel+BamHI to give pJ6018. Coomassie blue staining following SDS-PAGE failed to reveal a protein of the expected size that was present only in induced cultures of S. lividans 1326[pIJ6018] (Fig. 2B, upper panel; the identity of the 27-kDa protein apparent only in these extracts is not known). However, Western analysis using Ab raised to FGH identified a protein of approx. 20 kDa that co-migrated with FGH and that was absent from uninduced cultures of S. lividans 1326[pIJ6018], and from extracts of S. lividans 1326[pIJ6021] grown with and without Th (Fig. 2B, lower panel).

redD is the putative pathway-specific activator gene for the undecylprodigiosin biosynthetic pathway of S. coelicolor (Narva and Feitelson, 1990; Takano et al., 1992). pIJ6021 was cleaved with Ndel, 5’ extensions were filled in with PolIk, and the DNA was cut with BamHI. The vector fragment was ligated with a 1.44-kb blunt-redD-BamHI fragment to give pJ4123 (Fig. 1), in which the ATG start codon of an N-terminally extended redD ORF was positioned just downstream from the tipA RBS. Coomassie blue-staining following SDS-PAGE of the soluble fraction and pellet obtained after sonication of S. coelicolor JF1[pJ4123] that had been induced with Th, and of total protein extracts of the same culture, revealed a protein of approx. 32 kDa that was absent from extracts of uninduced cultures (Fig. 2C, upper panel). Western analysis using Ab raised to RedD (J.W., unpublished results) confirmed that the 32-kDa protein was RedD (Fig. 2C, lower panel); no such signal was detected in extracts of S. coelicolor JF1[pJ4123] grown without Th. A significant proportion of the RedD protein made in induced cultures appeared to be insoluble (Fig. 2C, upper panel, lanes S and P).
Fig. 1. Restriction maps of plasmids plJ6021 and plJ4123. Open circles indicate unique cloning sites present in the MCS; closed circles indicate that additional unmarked sites occur in the vectors; redD of plJ4123 contains unmarked ClaI and PvuII sites (one of each). The filled arrowhead indicates the direction of transcription from p\text{pa}. The tipA RBS and ATG start codon are underlined, and the open arrowhead indicates the site of cleavage by thrombin. The vectors were constructed using standard cloning procedures (Hopwood et al., 1985; Sambrook et al., 1989). Details of their constructions are available from the authors on request.

(c) plJ4123 as a vector for the production of His\textsubscript{6}-tagged proteins

The RedD protein produced from plJ4123 has an N-terminal extension derived from the 65-bp NcoI-NdeI segment of pET15b (Novagen, Madison, WI, USA). The presence of a His\textsubscript{6} tag within this extension greatly aided the subsequent purification of the RedD fusion protein by Ni\textsuperscript{2+}-affinity chromatography (J.W., unpublished results). To take advantage of this facility, plJ4123 can be cleaved with NdeI, or NdeI plus either BamHI or EcoRI, to generate a linearised replicon containing \textit{P}_{\text{tipA}} upstream from the sequence encoding the His\textsubscript{6} tag, which terminates at the unique NdeI site. A gene of interest with a NdeI site positioned to allow the production of a His-tagged fusion protein can then be inserted into the replicon, and the fusion protein readily purified by Ni\textsuperscript{2+}-affinity chromatography. Transformants of \textit{S. lividans} or \textit{S. coelicolor} containing uncut or religated vector produce enough RedD even in the absence of Th induction to yield intensely red colonies, providing a facile visual screen for recombinant clones.

(d) Concluding remarks

plJ6021 has proved effective in expressing three functionally diverse genes in \textit{S. lividans} or \textit{S. coelicolor}: a eukaryotic growth hormone (\textit{fgh}), a putative transcriptional activator (\textit{redD}) and a membrane-associated \(\beta\)-keto acyl synthase (\textit{tcmK}). It has also been used to express the \textit{whiB} (E. Vijgenboom, personal communication) and \textit{actII-ORF4} (F. Malpartida, personal communication) genes of \textit{S. coelicolor} in \textit{S. lividans}. While the level of \textit{fgh} expression was too low for detection by Coomassie blue staining, TcmK and RedD appeared to be made at levels of a few percent of total cell protein. Unlike TcmK, FGH and RedD were not detected by Western analysis prior to induction of \textit{P}_{\text{tipA}} with Th. The inability to detect basal levels of \textit{fgh} and \textit{redD} expression might reflect the rapid
Fig. 2. Expression of native and foreign genes in pIJ6021. SM, size markers; U, uninduced; I, induced; TP, total protein; S, soluble fraction obtained after sonication; P, pellet obtained after sonication; FGH, 0.1 μg of purified FGH. (A) Expression of tcmK in pIJ6021. The 1.7-kb Ndel-HindIII fragment of pIJ2232 that contains tcmK (Gramajo et al., 1991) was ligated with the 6-kb Ndel-XhoI and 1.8-kb XhoI-HindIII fragments of pIJ6021 to give pIJ6024 (the adjacent locations of the Ndel and HindIII sites of pIJ6021 appeared to prevent digestion by both enzymes, precluding simple insertion of the tcmK fragment in Ndel+HindIII-digested pIJ6021). (B) Expression of fgh in pIJ6021. 20 pmol of the 5’ primer 5’-CATGGATCCCATATGCAGCCGATCACCGAGAACCAGCGCCTGTTGTCC and of the 3’ primer 5’-CATGGATCCGGTACTTCTTGCGGGACAGG, and 10 ng of a pBluescript KS(+) (Stratagene, La Jolla, CA, USA) derivative containing the modified fgh coding sequence (Takano et al., 1992), were used to amplify the 35 cycles of the PCR (95°C for 30 s, 55°C for 30 s and 72°C for 1 min) in the presence of 10 mM Tris-HCl pH 8.3/2.5 mM MgCl2/50 mM KCl/5% (v/v) glycerol/0.1% (w/v) gelatin/200 μM of each dNTP/2.5 units of Taq polymerase (Boehringer-Mannheim). The amplified fragment was gel-purified, cleaved with BamHI, and inserted in the BamHI site of pIJ2925 (Janssen and Bibb, 1993) to give pIJ6107; the sequence of the modified fgh was confirmed by double-strand sequencing using the Promega TaqTrack Sequencing System. pIJ6107 was digested with Ndel + BamHI, the 550-bp fragment containing the modified fgh gel-purified and inserted in Ndel + BamHI-digested pIJ6021 to give pIJ6018. (C) Expression of redD in pIJ6021. Synthetic oligodeoxyribonucleotides, extending from the start codon of redD to a CiaI site located 27 nt into the redD coding sequence (Takano et al., 1992), were used to create a Ndel site overlapping the redD start codon. A 1.38-kb Ndel-redD-BamHI fragment was inserted in Ndel- and BamHI-cleaved pET15b (Novagen) to give pIJ4116, which has a unique NcoI site located 59-bp upstream from the Ndel site. pIJ4116 was digested with NcoI, 5’ extensions filled in with Pollk, and the DNA cut with BamHI to release a 1.44-kb blunt-Ndel-redD-BamHI fragment. pIJ6021 was cleaved with Ndel, 5’ extensions filled in with Pollk, the DNA cut with BamHI and ligated with the 1.44-kb fragment containing redD to give pIJ4123. S. lividans 1326 (Hopwood et al., 1985) or S. coelicolor strain JF1 (argA1, gusA1, redD42, actII-177, SCP1+, SCP2+; Feitelson and Hopwood, 1983) derivatives containing pIJ6021, pIJ6018, pIJ6024 or pIJ4123 were selected by flooding transformation plates with 1 ml of water containing 2 mg Km. After single colony purification and confirmation of the required construct by restriction analysis, derivatives were grown in 10 ml of YEME (Hopwood et al., 1985) containing 5 μg Km/ml in Universal (40 ml capacity) containers containing small stainless steel springs at 300 rpm at 30°C; transcription from pSC101 was induced after 12 h by addition of Th to a final concentration of 5 μg/ml. After a further 12 h of incubation, the cells were harvested by centrifugation. For the analysis of fgh and tcmK expression, the samples of mycelium were boiled in loading buffer (62.5 mM Tris-HCl pH 6.8/2% (w/v) SDS/10% (v/v) glycerol/5% (v/v) 2-mercaptoethanol/0.1% (w/v) bromophenol blue). For analysis of redD expression, mycelium was also disrupted by sonication, and samples of the soluble fraction and pellet boiled with equal volumes of 2 × loading buffer. Samples were fractionated by 0.1% SDS/12-14% (w/v) PAGE and protein bands visualised with Coomassie blue stain. Duplicate sets of samples were run on identical gels, transferred to nitrocellulose filters, and probed with 1:1000 dilutions of Ab raised in rabbits against FGH or a synthetic oligopeptide corresponding to TcmK (Gramajo et al., 1991), or with a 1:1000 dilution of Ab raised in a rat against RedD (J.W., unpublished data), as described by Burnette (1991). A goat anti-rabbit immunoglobulin G-alkaline phosphatase conjugate (Bethesda Research Laboratories) was used as the second Ab. The top panels show the Coomassie-blue-stained gels, and the lower panels show the results of the Western analyses. The nature of the cross-reacting proteins of approx. 50 kDa observed in the lower panels of B and C is not known.
degradation of their fusion transcripts or protein products, or differences in the avidity of their cognate Ab. Although Western analysis failed to detect RedD in extracts of uninduced S. coelicolor A3(2) JF1 [plJ4123], the cultures produced large quantities of undecylprodigiosin, indicating that some RedD protein was made. Thus, genes cloned in these vectors appear to be expressed at basal levels even in the absence of Th induction. This may reflect transcription initiating at pRIP2A, or elsewhere in the vector that is not completely terminated at t4.

Induction of pRIP2A requires tipA both in vitro (Holmes et al., 1993) and in vivo (T. Katoh and C.J.T., unpublished data). While tipA homologues apparently occur in many Streptomyces species, including the S. lividans and S. coelicolor strains used here, they are not present in all (E.T., unpublished data). Thus, to use these vectors in strains that lack tipA, the gene must be provided either by insertion in plJ6021 or plJ4123, or by introduction on a separate vector.

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